SEQUENCE LISTING

<110> IMMUCON INC.
SULLIVAN, Robert
BÉRUBÉ, Bruno
LÉGARÉ, Christine
GAUDREAULT, Christian

<120> ACROSOMAL SPERM PROTEIN AND USES THEREOF

<130> 13045-2PCT FC/ld

<150> US09/090,567
<151> 1998-06-08

<160> 7

<170> FastSEQ for Windows Version 3.0

<210> 1
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<222> (124)...(856)
<223> p26h cDNA

<400> 1

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agc atg aag ctg aat ttc act ggt ctc agg gct ctg gtg acc ggg gca       168
    Met Lys Leu Asn Phe Thr Gly Leu Arg Ala Leu Val Thr Gly Ala
     1               5                  10                  15

ggg aga ggg att ggg cga ggc act gcg aaa gcc ctg cat gcc tca gga       216
Gly Arg Gly Ile Gly Arg Gly Thr Ala Lys Ala Leu His Ala Ser Gly
                20                  25                  30

gcc aaa gtg gtg gcc gtg tca ctc atc aac gaa gac ctg gtc agc ctg       264
Ala Lys Val Val Ala Val Ser Leu Ile Asn Glu Asp Leu Val Ser Leu
            35                  40                  45

gcc aaa gag tgt ccg ggc ata gag cct gtg tgt gtg gac ctg ggt gac       312
Ala Lys Glu Cys Pro Gly Ile Glu Pro Val Cys Val Asp Leu Gly Asp
        50                  55                  60

tgg gag gcc aca gag aag gca ctg ggc cgt att ggc ccc gtg gac ctg       360
Trp Glu Ala Thr Glu Lys Ala Leu Gly Arg Ile Gly Pro Val Asp Leu
    65                  70                  75

ctg gtg aac aat gcg gcg gtg gcg cta gtg cag cct ttc ata cag tct       408
Leu Val Asn Asn Ala Ala Val Ala Leu Val Gln Pro Phe Ile Gln Ser
80                  85                  90                  95
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acc aag gag gtc ttt gac agg tcc ttc aat gtg aat gtg cgc tct gtg      456
Thr Lys Glu Val Phe Asp Arg Ser Phe Asn Val Asn Val Arg Ser Val
                100                 105                 110

ctg caa gtg tcc cag atg gta gcc aag ggc atg att aac cgt gga gtg      504
Leu Gln Val Ser Gln Met Val Ala Lys Gly Met Ile Asn Arg Gly Val
            115                 120                 125

gca gga tcc att gtc aac atc tcc agc atg gtg gcc tat gtc acc ttc      552
Ala Gly Ser Ile Val Asn Ile Ser Ser Met Val Ala Tyr Val Thr Phe
        130                 135                 140

cct ggt ctg gcc acg tac agc tcc acc aag ggt gct ata acc atg ctg      600
Pro Gly Leu Ala Thr Tyr Ser Ser Thr Lys Gly Ala Ile Thr Met Leu
    145                 150                 155

acc aaa gcc atg gcc atg gag ctg gga cca tac aag atc cgg gtg aac      648
Thr Lys Ala Met Ala Met Glu Leu Gly Pro Tyr Lys Ile Arg Val Asn
160                 165                 170                 175

tct gta aac cct acc gtg gtg ctg act gac atg ggc aag aaa gtc tct      696
Ser Val Asn Pro Thr Val Val Leu Thr Asp Met Gly Lys Lys Val Ser
                180                 185                 190

gca gac ccg gaa ttt gcc aag aag ctc aag gag cgc cac cca ctg agg      744
Ala Asp Pro Glu Phe Ala Lys Lys Leu Lys Glu Arg His Pro Leu Arg
            195                 200                 205

aag ttc gca gag gtg gag gac gtg gtc aac agc atc ctc ttc ctg ctc      792
Lys Phe Ala Glu Val Glu Asp Val Val Asn Ser Ile Leu Phe Leu Leu
        210                 215                 220

agc gac agc agc gcc tct acc agc ggc tct ggc atc ctg gtg gac gct      840
Ser Asp Ser Ser Ala Ser Thr Ser Gly Ser Gly Ile Leu Val Asp Ala
    225                 230                 235

ggt tac ctg gcc tcc t agacggccca ggtgcagggg actcctggag acttccctgg    896
Gly Tyr Leu Ala Ser
240

cctcaccctt acatcaagac cccgccttca acccaaccca ataattttgt tcgaatcctg    956
tagagcccca ccccacacac atccatcccc aactttagac tccgggatcc cgccattcca   1016
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Lys Val Val Ala Val Ser Leu Ile Asn Glu Asp Leu Val Ser Leu Ala
        35                  40                  45
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    50                  55                  60
Glu Ala Thr Glu Lys Ala Leu Gly Arg Ile Gly Pro Val Asp Leu Leu
65                  70                  75                  80
Val Asn Asn Ala Ala Val Ala Leu Val Gln Pro Phe Ile Gln Ser Thr
                85                  90                  95
Lys Glu Val Phe Asp Arg Ser Phe Asn Val Asn Val Arg Ser Val Leu
            100                 105                 110
Gln Val Ser Gln Met Val Ala Lys Gly Met Ile Asn Arg Gly Val Ala
        115                 120                 125
Gly Ser Ile Val Asn Ile Ser Ser Met Val Ala Tyr Val Thr Phe Pro
    130                 135                 140
Gly Leu Ala Thr Tyr Ser Ser Thr Lys Gly Ala Ile Thr Met Leu Thr
145                 150                 155                 160
Lys Ala Met Ala Met Glu Leu Gly Pro Tyr Lys Ile Arg Val Asn Ser
                165                 170                 175
Val Asn Pro Thr Val Val Leu Thr Asp Met Gly Lys Lys Val Ser Ala
            180                 185                 190
Asp Pro Glu Phe Ala Lys Lys Leu Lys Glu Arg His Pro Leu Arg Lys
        195                 200                 205
Phe Ala Glu Val Glu Asp Val Val Asn Ser Ile Leu Phe Leu Leu Ser
    210                 215                 220
Asp Ser Ser Ala Ser Thr Ser Gly Ser Gly Ile Leu Val Asp Ala Gly
225                 230                 235                 240
Tyr Leu Ala Ser
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<211> 912
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cgggtggtgg ctgtgagccg gactcaggcg gatcttgaca gccttgtccg cgagtgcccg    240
gggatagaac ccgtgtgcgt ggacctgggt gactgggagg ccaccgagcg ggcgctgggc    300
agcgtgggcc ccgtggacct gctggtgaac aacgccgctg tcgccctgct gcagcccttc    360
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caggtgtcgc agattgtggc caggggctta atagcccggg gagtaccagg ggccatcgtg    480
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gagcacgtgg tgaacgccat cctctttctg ctgagtgacc gaagtggcat gaccacgggt    780
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<210> 4
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<212> PRT
<213> Artificial Sequence

<220>
<223> P34 antigenic fragment

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<210> 5
<211> 11
<212> PRT
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<400> 5
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1 5 10

<210> 6
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<212> DNA
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<400> 6
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<210> 7
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<212> DNA
<213> Artificial Sequence

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<223> cDNA for use as primer

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gcaactgagc agactaggag g 21

SEQUENCE LISTING

<110> Robert Sullivan et al.

<120> ACROSOMAL SPERM PROTEIN AND USES THEREOF

<130> 13045-2US-1 FC/JM

<150> US09/090,567
<151> 1998-06-08

<150> PCT/CA99/00437
<151> 1998-05-13

<160> 7

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 1081
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<220>
<221> CDS
<222> (124)...(856)
<223> p26h cDNA

<400> 1

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tgagcagatc aaccttaacc tcagcccctc cctcgccac aggaggacac tggtgtcagc      120
agc atg aag ctg aat ttc act ggt ctc agg gct ctg gtg acc ggg gca      168
    Met Lys Leu Asn Phe Thr Gly Leu Arg Ala Leu Val Thr Gly Ala
     1               5                  10                  15

ggg aga ggg att ggg cga ggc act gcg aaa gcc ctg cat gcc tca gga      216
Gly Arg Gly Ile Gly Arg Gly Thr Ala Lys Ala Leu His Ala Ser Gly
                20                  25                  30

gcc aaa gtg gtg gcc gtg tca ctc atc aac gaa gac ctg gtc agc ctg      264
Ala Lys Val Val Ala Val Ser Leu Ile Asn Glu Asp Leu Val Ser Leu
            35                  40                  45

gcc aaa gag tgt ccg ggc ata gag cct gtg tgt gtg gac ctg ggt gac      312
Ala Lys Glu Cys Pro Gly Ile Glu Pro Val Cys Val Asp Leu Gly Asp
        50                  55                  60

tgg gag gcc aca gag aag gca ctg ggc cgt att ggc ccc gtg gac ctg      360
Trp Glu Ala Thr Glu Lys Ala Leu Gly Arg Ile Gly Pro Val Asp Leu
    65                  70                  75

ctg gtg aac aat gcg gcg gtg gcg cta gtg cag cct ttc ata cag tct      408
Leu Val Asn Asn Ala Ala Val Ala Leu Val Gln Pro Phe Ile Gln Ser
80                  85                  90                  95
```

```
acc aag gag gtc ttt gac agg tcc ttc aat gtg aat gtg cgc tct gtg      456
Thr Lys Glu Val Phe Asp Arg Ser Phe Asn Val Asn Val Arg Ser Val
                100                 105                 110

ctg caa gtg tcc cag atg gta gcc aag ggc atg att aac cgt gga gtg      504
Leu Gln Val Ser Gln Met Val Ala Lys Gly Met Ile Asn Arg Gly Val
            115                 120                 125

gca gga tcc att gtc aac atc tcc agc atg gtg gcc tat gtc acc ttc      552
Ala Gly Ser Ile Val Asn Ile Ser Ser Met Val Ala Tyr Val Thr Phe
        130                 135                 140

cct ggt ctg gcc acg tac agc tcc acc aag ggt gct ata acc atg ctg      600
Pro Gly Leu Ala Thr Tyr Ser Ser Thr Lys Gly Ala Ile Thr Met Leu
    145                 150                 155

acc aaa gcc atg gcc atg gag ctg gga cca tac aag atc cgg gtg aac      648
Thr Lys Ala Met Ala Met Glu Leu Gly Pro Tyr Lys Ile Arg Val Asn
160                 165                 170                 175

tct gta aac cct acc gtg gtg ctg act gac atg ggc aag aaa gtc tct      696
Ser Val Asn Pro Thr Val Val Leu Thr Asp Met Gly Lys Lys Val Ser
                180                 185                 190

gca gac ccg gaa ttt gcc aag aag ctc aag gag cgc cac cca ctg agg      744
Ala Asp Pro Glu Phe Ala Lys Lys Leu Lys Glu Arg His Pro Leu Arg
            195                 200                 205

aag ttc gca gag gtg gag gac gtg gtc aac agc atc ctc ttc ctg ctc      792
Lys Phe Ala Glu Val Glu Asp Val Val Asn Ser Ile Leu Phe Leu Leu
        210                 215                 220

agc gac agc agc gcc tct acc agc ggc tct ggc atc ctg gtg gac gct      840
Ser Asp Ser Ser Ala Ser Thr Ser Gly Ser Gly Ile Leu Val Asp Ala
    225                 230                 235

ggt tac ctg gcc tcc t agacggccca ggtgcagggg actcctggag acttccctgg    896
Gly Tyr Leu Ala Ser
240

cctcaccctt acatcaagac cccgccttca acccaaccca ataatttttgt tcgaatcctg    956
tagagccccca ccccacacac atccatcccc aactttagac tccgggatcc cgccattcca   1016
taccagctat gctgagataa tttgattaaa taagtatccc aaaccacaaa aaaaaaaaaa   1076
aaaaa                                                               1081
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<210> 2
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Met Lys Leu Asn Phe Thr Gly Leu Arg Ala Leu Val Thr Gly Ala Gly
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Arg Gly Ile Gly Arg Gly Thr Ala Lys Ala Leu His Ala Ser Gly Ala
            20                  25                  30
```

```
Lys Val Val Ala Val Ser Leu Ile Asn Glu Asp Leu Val Ser Leu Ala
        35                  40                  45
Lys Glu Cys Pro Gly Ile Glu Pro Val Cys Val Asp Leu Gly Asp Trp
    50                  55                  60
Glu Ala Thr Glu Lys Ala Leu Gly Arg Ile Gly Pro Val Asp Leu Leu
65                  70                  75                  80
Val Asn Asn Ala Ala Val Ala Leu Val Gln Pro Phe Ile Gln Ser Thr
                85                  90                  95
Lys Glu Val Phe Asp Arg Ser Phe Asn Val Asn Val Arg Ser Val Leu
            100                 105                 110
Gln Val Ser Gln Met Val Ala Lys Gly Met Ile Asn Arg Gly Val Ala
        115                 120                 125
Gly Ser Ile Val Asn Ile Ser Ser Met Val Ala Tyr Val Thr Phe Pro
    130                 135                 140
Gly Leu Ala Thr Tyr Ser Ser Thr Lys Gly Ala Ile Thr Met Leu Thr
145                 150                 155                 160
Lys Ala Met Ala Met Glu Leu Gly Pro Tyr Lys Ile Arg Val Asn Ser
                165                 170                 175
Val Asn Pro Thr Val Val Leu Thr Asp Met Gly Lys Lys Val Ser Ala
            180                 185                 190
Asp Pro Glu Phe Ala Lys Lys Leu Lys Glu Arg His Pro Leu Arg Lys
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Phe Ala Glu Val Glu Asp Val Val Asn Ser Ile Leu Phe Leu Leu Ser
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Asp Ser Ser Ala Ser Thr Ser Gly Ser Gly Ile Leu Val Asp Ala Gly
225                 230                 235                 240
Tyr Leu Ala Ser
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aagggtgccc tggacatgct gaccaaggtg atggcctag agctcgggcc ccacaagatc     600
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tccactttgc cggtggaaag gggcttctgg gcctgctgag ctccctccac acacctcaag     840
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